

IN THE CLAIMS

In accordance with the revised format for claim amendments, all claims are shown below. Please amend the claims as follows:

1. (Currently Amended) A nucleic acid molecule having a nucleic acid sequence that encodes a linker region of exoglucanase, said nucleic acid sequence comprising the nucleotide sequence: of SEQ ID NO: 3-5' GGCGGAAACCCGCCTGGCACCAACC 3'.
2. (Original) The nucleic acid molecule of claim 1 wherein said exoglucanase is further defined as a cellobiohydrolase.
3. (Original) The nucleic acid molecule of claim 1 wherein said exoglucanase is further defined as a 1,4- $\beta$ -cellobiohydrolase.
4. (Currently Amended) The nucleic acid molecule of claim 1 whereas said nucleic acid sequence is further defined as comprising SEQ ID NO: 19.
5. (Cancelled) ~~CCTCCCCGGCGGAAACCCGCCTGGCACCAACCACCCGCCGCCA 3'~~.
6. (Original) A nucleic acid molecule having a nucleic acid sequence encoding a variant cellobiohydrolase, said nucleic acid sequence comprising a linker region sequence having a length of from about 20 nucleotides to about 50 nucleotides linker region, between a catalytic domain and a cellulose binding domain (CBD).
7. (Original) The nucleic acid molecule of claim 5 wherein the variant cellobiohydrolase is further defined as having enhanced thermostability.
8. (Original) The nucleic acid molecule of claim 5 wherein the variant cellobiohydrolase is further defined as an 1,4  $\beta$ -cellobiohydrolase.
9. (Original) The nucleic acid molecule of claim 5 wherein the cellobiohydrolase is further defined as having reduced end-product inhibition.
10. (Original) The nucleic acid molecular of claim 5 wherein the linker region sequence has a length of about 24 nucleotides.
11. (Original) A method for making an active exoglucanase in a eukaryotic heterologous host, the method comprising reducing glycosylation of the exoglucanase, wherein reducing comprises replacing an N-glycosylation site amino acid residue with non-glycosyl accepting amino acid residue.

12. (Original) The method of claim 10, wherein the N-glycosylation site amino acid residues include asparagines 45, 270, or 384 of Table 4 and the non-glycosyl accepting amino acid residue includes alanine.
13. (Original) The method of claims 10, wherein replacing comprises site-directed mutagenesis.
14. (Original) The methods of claims 10, wherein the exoglucanase comprises a cellobiohydrolase.
15. (Currently Amended) An exoglucanase, comprising of the sequence change of Table 4, N45A 5' GGACTCACGCTACGGCCAGCAGCACGACTGC 3' SEQ ID NO: 20.
16. (Currently Amended) An exoglucanase, comprising of the sequence change of Table 4, N270A, 5' CCCATACCGGCCTGGGCCACCAGGCTTCTACGGCCC 3' SEQ ID NO: 21.
17. (Currently Amended) An exoglucanase, comprising of the sequence change of Table 4, N384A, 5'  
GGACTCCACCTACCCGACAGCCGAGACCTCCTCCACACCCG 3' SEQ ID NO: 22.
18. (Currently Amended) An exoglucanase, comprising a combination of claims 14,15,16,17.

IN THE FIGURES

Figure 1. Coding sequence for the *cbh1* gene (SEQ ID NO: 4). Small case letters represent the signal sequence, large case letters the catalytic domain, bolded italics the linker region, and large case underlined the cellulose-binding domain.

atgtatcggaagtggccgtatcggccttggccacagctgtgcAGTCGGCCTGCACCTCCAATCGGAACCTCAC  
CCGCCTCTGACATGGCAGAAATGCTCGTCTGGTGGCACGTGCACCAACAGACAGGCTCCGTG  
GTCATCGACGCCA**ACTGGCGCTGGACTCACGCTACGAACAGCAGCACGA**ACTGCTACGATGG  
CAACACTTGGAGCTCGACCCTATGTCTGACAACAGAGACCTGCGCAAGAA**ACTGCTGTCTGG**A  
CGGTGCCGCTACCGTCCACGTACGGAGTTACACGAGCGGTAACAGCCTCTCCATTGGCTT  
TGTCA**CCCAGTCTGCGCAGAAGAACGTTGGCGCTCGCCTTACCTTATGGCGAGCGACACGAC**  
CTACCAGGAATT**CACCTGCTTGGCAACGAGTTCTCTTCGATGTTGATTTCGCAGCTGCCG**  
TGC**GGCTGAACGGAGCTCTACTTCGTGTCCATGGACGCGGATGGTGGCGTGAGCAAGTAT**  
CCCACCAACACCGCTGGCG**CCAAGTACGGCACGGGTACTGTGACAGCCAGTGTCCCCCGCGA**  
TCTGAAGTT**CATCAATGGCCAGGCCAACGTTGAGGGCTGGAGGCCGTATCCAACAAACGCGA**  
ACACGGGCATTGGAGGACACGGAA**GCTGCTCTGAGATGGATATCTGGGAGGCCA**ACTCC  
ATCTCCGAGGCTT**ACCCCCCACCTGCACGACTGTCGGCAGGAGATCTGCGAGGGTGAT**  
GGGTGCGGCG**GAACTTACTCCGATAACAGATATGGCGGACTTGCATCCGATGGCTGCGA**  
CTGGAA**CCCATACCGCTGGCAACACCAGCTTCTACGGCCCTGGCTCAAGCTTACCTCGA**  
TACCACCAAGAA**ATTGACCGTTGTCACCCAGTTGAGACGTCGGGTGCCATCAACCGATACTA**  
TGTCCAGA**ATGGCGTCACTTCCAGCAGCCAACGCGGAGCTGGTAGTTACTCTGGCAACGA**  
GCTCAACG**ATGATTACTGCACAGCTGAGGAGGCAGAATTGGCGGATCCTCTTCAGACAA**  
GGGCGG**CCTGACTCAAGAAGGCTACCTCTGGCGCATGGTCTGGTCATGAGTCTGTG**  
GGATGATT**ACTACGCCAACATGCTGGCTGGACTCCACCTACCCGACAAACGAGACCTCCTC**  
CACACCCGGT**GCGTGC**CGGAAG**CTGCTCCACCAAGCTCCGGTGTCCCTGCTCAGGT**CGAATC  
TCAGT**CTCCCAACGCCAAGGT**CACCT**TCTCCAACATCAAGTTGGACCCATTGGCAGCACC**GG  
CAAC**CCTAGCGCGGCAACCCCTCCCCGGGAAACCCGCTGGCACCACCA**CCACCCGGC**CCCC**  
**AGCCACTACCAACTGGAAAGCTCTCCGGACCTACCCAGTCTCACTACGCCAGTGC**GGCG**TATT**  
**GGCTACAGCGGCCCCACGGTCTGCCAGCGGCACAAC**TTGCCAGGT**CCTGAACCTTACTAC**  
**TCTCAGTGCCTGTAAAGCTCC**

Figure 4. Coding sequence, SEQ ID NO: 19, for the linker region of the *cbh1* gene, SEQ ID NO: 4, showing additional proline nucleotides that effect conformation of the linker region in the protein structure.

